

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma
Yasuaki Ito
Ryo Fujii

7,2390
(ii) TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof

(iii) NUMBER OF SEQUENCES: 61

(iv) CORRESPONDENCE ADDRESS:

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(B) 101 Federal Street
(C) CITY: BOSTON
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(E) COUNTRY: USA
(F) ZIP: 02209

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

E1
(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/461,436
(B) FILING DATE: 14-DECEMBER-1999
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/513,974
(B) FILING DATE: 14-SEP-1995

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(B) FILING DATE: 11-AUG-1994

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(B) FILING DATE: 11-AUG-1994

(viii) ATTORNEY/AGENT INFORMATION

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is A, G, C, or T; S is G or C;
M is A or C; Y is T or C."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGTGGSCMTS STGGGCAACN YCCTG

25

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is A, G, C, or T; W is A or T;
R is A or G; K is G or T."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GTNGWRRGGC ANCCAGCAGA KGGCAAA 27

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is inosine; S is G or C;
Y is C or T; M is A or C; R is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCGCSGCYM TNRGYATGGA YCGNTAT 27

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is inosine; R is A or G;
W is T or A; S is G or C; M is A or C."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CATGTRGWAG GGAANCCAGS AMANRARRAA 30

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:
(D) OTHER INFORMATION: /note= N is inosine; Y is C or T;
R is A or G; S is G or C; M is A or C; V is A, C or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTGACYGYTC TNRSNRYTGA CMGVTAC 27

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

E1 (ix) FEATURE:
(D) OTHER INFORMATION: /note= N is inosine; Y is C or T;
R is A or G; S is G or C; M is A or C; V is A, C or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTGACYGYTC TNRSNRYTGA CMGVTAT 27

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:
(D) OTHER INFORMATION: /note= N is inosine; S is G or C;
Y is C or T; M is A or C; R is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTCGCSGCMY TNRGYATGGA YCGNTAC 27

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is inosine; R is A or G;
S is G or C; Y is C or T."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GATGTGRTAR GGSRNCCAAC AGANGRYAAA 30

E1
(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is inosine; R is A or G;
S is G or C; Y is C or T."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GATGTGRTAR GGSRNCCAAC AGANGRYGAA 30

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:
 (D) OTHER INFORMATION: /note= N is inosine; S is G or C;
 Y is C or T; W is A or T; H is A, C or T."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GYCACCAACN WSTTCATCCT SWNHCTG 27

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:
 (D) OTHER INFORMATION: /note= N is inosine; R is A or G;
 S is G or C."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ASNSANRAAG SARTAGANGA NRGGR TT 27

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:
 (D) OTHER INFORMATION: /note= N is inosine; S is G or C;
 K is G or T; M is A or C."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TGNTSSTKMT NGSNGTKGTN GGNAA 25

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is inosine; Y is C or T;
K is G or T; W is A or T."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AYCKGTAYCK GTCCANKGWN ATKGC 25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is inosine; K is G or T;
S is G or C; Y is C or T; R is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CATKKCCSTG GASAGNTAYN TRGC 24

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:
(D) OTHER INFORMATION: /note= N is inosine; W is A or T;
S is G or C; K is G or T; R is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GWGGGGSAKC CAGCASANGG CRAA

24

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:
(D) OTHER INFORMATION: /note= N at position 6, 9, 10 & 12 = inosine;
N at position 15 = A, G, C, or T; R is A or G; Y is C or T."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ARYYTNGCNN TNGCNGAY

18

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:
(D) OTHER INFORMATION: /note= N at position 1, 4, & 6 = inosine;
N at position 13, 15, 16 & 18 = A, G, C, or T; R is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

NGGNANCCAR CANANNRNRA A

21

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (D) OTHER INFORMATION: /note= N is inosine; S is G or C; R is A or G;
W is A or T; M is A or C."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCTSNTNRN SATGWSTGTG GANMGNT

27

E1 (2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (D) OTHER INFORMATION: /note= N is inosine, W is A or T,
S is G or C, M is A or C, Y is C or T, R is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GAWSNTGMYN ANRTGGWAGG GNANCCA

27

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TAGTGTGTGG AGTCGTGTGG CTGGCTG 27

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

AGTCTTTGCT GCCACAGGCA TCCAGCG 27

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CAAGCCAGTA AGGCTATGAA GGGCAGCAAG 30

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

E1

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ACAGGACCTG CTGGGCCATC CTGGCGACAC A 31

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91
(B) TYPE: Amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn
1 5 10 15
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
20 25 30
Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
35 40 45
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr
50 55 60
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
65 70 75 80
Val Val Leu Val His Pro Leu Arg Arg Arg Ile
85 90

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59
(B) TYPE: Amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu
1 5 10 15
Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly

	20		25		30										
Cys	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Arg
		35					40					45			
Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val					
	50					55									

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

E1

Met	Ala	Ser	Ser	Thr	Thr	Arg	Gly	Pro	Arg	Val	Ser	Asp	Leu	Phe	Ser
1				5					10					15	
Gly	Leu	Pro	Pro	Ala	Val	Thr	Thr	Pro	Ala	Asn	Gln	Ser	Ala	Glu	Ala
			20					25					30		
Ser	Ala	Gly	Asn	Gly	Ser	Val	Ala	Gly	Ala	Asp	Ala	Pro	Ala	Val	Thr
		35					40					45			
Pro	Phe	Gln	Ser	Leu	Gln	Leu	Val	His	Gln	Leu	Lys	Gly	Leu	Ile	Val
	50					55					60				
Leu	Leu	Tyr	Ser	Val	Val	Val	Val	Val	Gly	Leu	Val	Gly	Asn	Cys	Leu
65					70					75				80	
Leu	Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Arg	Leu	His	Asn	Val	Thr	Asn
				85					90					95	
Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu	Met	Cys	Thr	Ala
			100					105					110		
Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val
		115					120					125			
Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Pro	Val	Thr
	130					135					140				
Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr
145					150					155					160
Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser
				165					170					175	
Ala	Tyr	Ala	Val	Leu	Ala	Ile	Trp	Ala	Leu	Ser	Ala	Val	Leu	Ala	Leu

180 185 190
 Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
 195 200 205
 Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu
 210 215 220
 Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
 225 230 235 240
 Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val
 245 250 255
 Val Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
 260 265 270
 Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Ala
 275 280 285
 Val Cys Trp Leu Pro Leu His Val Phe Asn Leu Leu Arg Asp Leu Asp
 290 295 300
 Pro His Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys
 305 310 315 320
 His Trp Leu Ala Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala
 325 330 335
 Trp Leu His Asp Ser Phe Arg Glu Glu Leu Arg Lys Leu Leu Val Ala
 340 345 350
 Trp Pro Arg Lys Ile Ala Pro His Gly Gln Asn Met Thr Val Ser Val
 355 360 365
 Val Ile
 370

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu Tyr Asn Val Thr Asn
 1 5 10 15
 Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala

20 25 30
 Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
 35 40 45
 Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Ala Val Thr
 50 55 60
 Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
 65 70 75 80
 Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser
 85 90 95
 Ala Tyr Ala Val Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu
 100 105 110
 Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
 115 120 125
 Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu
 130 135 140
 Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
 145 150 155 160
 E1 Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu Arg Asn Arg Val
 165 170 175
 Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
 180 185 190
 Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val
 195 200 205

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser
 1 5 10 15
 Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu
 20 25 30
 Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val

35	40	45
Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Ile		
50	55	60
Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala		
65	70	75 80
Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val		
85	90	95
Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg		
100	105	110
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val		
115	120	125

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGCACAACG TGACGAACTT CCTCATCGGC	60
AACCTGGCCT TGTCCGACGT GCTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT	120
GCCTTCGAGC CACGCGGCTG GGTGTTCTGGC GGC GGCCTGT GCCACCTGGT CTTCTTCCTG	180
CAGCCGGTCA CCGTCTATGT GTCGGTGTTT ACGCTCACCA CCATCGCAGT GGACCGGTAC	240
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATC	273

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGCCTGCTGC TGGTCACCTA CCTGCTCCCT CTGCTGGTCA TCCTCCTGTC TTACGTCCGG	60
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GTGTCAGTGA AGCTCCGCAA CCGCGTGGTG CCGGGCTGCG TGACCCAGAG CCAGGCCGAC 120
 TGGGACCGCG CTCGGCGCCG GCGCACCTTC TGCTTGCTGG TGGTGGTCGT GGTGGTG 177

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGCCTCAT CGACCACTCG GGGCCCCAGG GTTCTGACT TATTTTCTGG GCTGCCGCCG 60
 GCGGTCACAA CTCCCGCCAA CCAGAGCGCA GAGGCCTCGG CGGGCAACGG GTCGGTGGCT 120
 GGCGCGGACG CTCCAGCCGT CACGCCCTTC CAGAGCCTGC AGCTGGTGCA TCAGCTGAAG 180
 GGGCTGATCG TGCTGCTCTA CAGCGTCGTG GTGGTCGTGG GGCTGGTGGG CAACTGCCTG 240
 CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGCACAACG TGACGAACTT CCTCATCGGC 300
 AACCTGGCCT TGTCCGACGT GTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT 360
 GCCTTCGAGC CACGCGGCTG GGTGTTCTGGC GCGGGCCTGT GCCACCTGGT CTTCTTCCTG 420
 CAGCCGGTCA CCGTCTATGT GTCGGTGTTT ACGCTCACCA CCATCGCAGT GGACCGCTAC 480
 GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG 540
 CTGGCCATCT GGGCGCTGTC CGCGGTGCTG GCGCTGCCCC CCGCCGTGCA CACCTATCAC 600
 GTGGAGCTCA AGCCGCACGA CGTGCGCCTC TGCAGGAGT TCTGGGGCTC CCAGGAGCGC 660
 CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC 720
 ATCCTCCTGT CTTACGTCCG GGTGTCAGTG AAGCTCCGCA ACCGCGTGGT GCCGGGCTGC 780
 GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGCACCTT CTGCTTGCTG 840
 GTGGTGGTCG TGGTGGTGTT CGCCGTCTGC TGGCTGCCGC TGCACGTCTT CAACCTGCTG 900
 CGGGACCTCG ACCCCCACGC CATCGACCCT TACGCCTTTG GGCTGGTGCA GCTGCTCTGC 960
 CACTGGCTCG CCATGAGTTC GGCCTGCTAC AACCCTTCA TCTACGCCTG GCTGCACGAC 1020
 AGCTTCCGCG AGGAGCTGCG CAAACTGTTG GTCGCTTGGC CCCGCAAGAT AGCCCCCAT 1080
 GGCCAGAATA TGACCGTCAG CGTGGTCATC 1110

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

E1

CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGTACAACG TGACGAATTT CCTCATCGGC	60
AACCTGGCCT TGTCCGACGT GTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT	120
GCCTTCGAGC CACGCGGCTG GGTGTTCTGGC GGCGGCCTGT GCCACCTGGT CTTCTTCCTG	180
CAGGCGGTCA CCGTCTATGT GTCGGTGTTT ACGCTCACCA CCATCGCAGT GGACCGCTAC	240
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG	300
CTGGCCATCT GGGTGCTGTC CGCGGTGCTG GCGCTGCCCC CCGCCGTGCA CACCTATCAC	360
GTGGAGCTCA AGCCGCACGA CGTGCGCCTC TGCAGGAGT TCTGGGGCTC CCAGGAGCGC	420
CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC	480
ATCCTCCTGT CTTACGCCCC GGTGTCAGTG AAGCTCCGCA ACCGCGTGGT GCCGGGCCGC	540
GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGCACCTT CTGCTTGCTG	600
GTGGTGGTCG TGGTGGTG	618

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTGGTTCTGG TGCACCCGCT ACGTCGGCGC ATTTCACTGA GGCTCAGCGC CTACGCGGTG	60
CTGGGCATCT GGGCTCTATC TGCAGTGCTG GCGCTGCCGG CCGCGGTGCA CACCTACCAT	120

GTGGAGCTCA AGCCCCACGA CGTGAGCCTC TCGAGGAGT TCTGGGGCTC GCAGGAGCGC 180
 CAACGCCAGA TCTACGCCTG GGGGCTGCTT CTGGGCACCT ATTTGCTCCC CCTGCTGGCC 240
 ATCCTCCTGT CTTACGTACG GGTGTCAGTG AAGCTGAGGA ACCGCGTGGT GCCTGGCAGC 300
 GTGACCCAGA GTCAAGCTGA CTGGGACCGA GCGCGTCGCC GCCGCACTTT CTGTCTGCTG 360
 GTGGTGGTGG TGGTAGTG 378

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Val Cys His Val Ile Phe Lys Asn Gln Arg Met His Ser Ala Thr Ser
 1 5 10 15
 Leu Phe Ile Val Asn Leu Ala Val Ala Asp Ile Met Ile Thr Leu Ile
 20 25 30
 Asn Thr Pro Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp Ile Phe
 35 40 45
 Gly Lys Gly Met Cys His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu
 50 55 60
 His Val Ser Ala Leu Thr
 65 70

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Pro Ala Asp Leu Phe Trp Lys Asn Leu Asp Leu Pro Thr Phe Ile
 1 5 10 15

Leu Leu Asn Ile Leu Pro Leu Leu Ile Ile Ser Val Ala Tyr Val Arg
 20 25 30
 Val Thr Lys Lys Leu Trp Leu Cys Asn Met Ile Val Asp Val Thr Thr
 35 40 45
 Glu Gln Tyr Phe Ala Leu Arg Pro Lys Lys Lys Lys Thr Ile Lys Met
 50 55 60
 Leu Met Leu Val Val Val Leu
 65 70

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTCTGTCATG TCATCTTCAA GAACCAGCGA ATGCACTCGG CCACCAGCCT CTTTCATCGTC 60
 AACCTGGCAG TTGCCGACAT AATGATCACG CTGCTCAACA CCCCCTTCAC TTTGGTTCGC 120
 TTTGTGAACA GCACATGGAT ATTTGGGAAG GGCATGTGCC ATGTCAGCCG CTTTGCCCAG 180
 TACTGCTCAC TGCACGTCTC AGCACTGACA 210

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAGCCAGCTG ACCTCTTCTG GAAGAACCTG GACTTGCCCA CCTTCATCCT GCTCAACATC 60
 CTGCCCCTCC TCATCATCTC TGTGGCCTAC GTTCGTGTGA CCAAGAACT GTGGCTGTGT 120
 AATATGATTG TCGATGTGAC CACAGAGCAG TACTTTGCCC TCGGGCCCAA AAAGAAGAAG 180
 ACCATCAAGA TGTTGATGCT GGTGGTAGTC CTC 213

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ala Ser Trp His Lys Arg Gly Gly Arg Arg Ala Ala Trp Val Val Cys
 1 5 10 15
 Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu Pro Thr Ala Val
 20 25 30
 Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val Cys Tyr Asp Leu
 35 40 45
 Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr Gly Met Ala Leu
 50 55 60
 Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu Leu Ala Cys Tyr
 65 70 75 80
 Cys Arg Met Ala Arg Arg Leu Cys Arg Gln Asp Gly Pro Ala Gly Pro
 85 90 95
 Val Ala Gln Glu Arg Arg Ser Lys Ala Ala Arg Met Ala Val Val Val
 100 105 110
 Ala Ala Val
 115

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Glu Gln Asp Asn Gly Thr Ile Gln Ala Pro Gly Leu Pro Pro Thr
 1 5 10 15

Thr Cys Val Tyr Arg Glu Asp Phe Lys Arg Leu Leu Leu Thr Pro Val
 20 25 30
 Tyr Ser Val Val Leu Val Val Gly Leu Pro Leu Asn Ile Cys Val Ile
 35 40 45
 Ala Gln Ile Cys Ala Ser Arg Arg Thr Leu Thr Arg Ser Ala Val Tyr
 50 55 60
 Thr Leu Asn Leu Ala Leu Ala Asp Leu Met Tyr Ala Cys Ser Leu Pro
 65 70 75 80
 Leu Leu Ile Tyr Asn Tyr Ala Arg Gly Asp His Trp Pro Phe Gly Asp
 85 90 95
 Leu Ala Cys Arg Phe Val Arg Phe Leu Phe Tyr Ala Asn Leu His Gly
 100 105 110
 Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly Ile
 115 120 125
 Cys His Pro Leu Ala Ser Trp His Lys Arg Gly Gly Arg Arg Ala Ala
 130 135 140
 Trp Val Val Cys Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu
 145 150 155 160
 Pro Thr Ala Val Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val
 165 170 175
 Cys Tyr Asp Leu Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr
 180 185 190
 Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu
 195 200 205
 Leu Ala Cys Tyr Cys Arg Met Ala Arg Arg Leu Cys Arg Gln Asp Gly
 210 215 220
 Pro Ala Gly Pro Val Ala Gln Glu Arg Arg Ser Lys Ala Ala Arg Met
 225 230 235 240
 Ala Val Val Val Ala Ala Val Phe Ala Ile Ser Phe Leu Pro Phe His
 245 250 255
 Ile Thr Lys Thr Ala Tyr Leu Ala Val Arg Ser Thr Pro Gly Val Ser
 260 265 270
 Cys Pro Val Leu Glu Thr Phe Ala Ala Ala Tyr Lys Gly Thr Arg Pro
 275 280 285
 Phe Ala Ser Val Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr
 290 295 300
 Gln Gln Lys Phe Arg Arg Gln Pro His Asp Leu Leu Gln Arg Leu Thr
 305 310 315 320

E1

Ala Lys Trp Gln Arg Gln Arg Val
325

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCTTCCTGGC ACAAGCGTGG AGGTCGCCGT GCTGCTTGGG TAGTGTGTGG AGTCGTGTGG 60
 CTGGCTGTGA CAGCCCAGTG CCTGCCCACG GCAGTCTTTG CTGCCACAGG CATCCAGCGC 120
 AACCGCACTG TGTGCTACGA CCTGAGCCCA CCCATCCTGT CTA CTGCTA CCTGCCCTAT 180
 GGTATGGCCC TCACGGTCAT CGGCTTCTTG CTGCCCTTCA TAGCCTTACT GGCTTGTTAT 240
 TGTCGCATGG CCCGCCGCCT GTGTCGCCAG GATGGCCCAG CAGGTCCTGT GGCCCAAGAG 300
 CGGCGCAGCA AGGCGGCTCG TATGGCTGTG GTGGTGGCAG CTGTC 345

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGGAGCAGG ACAATGGCAC CATCCAGGCT CCAGGCTTGC CGCCCACCAC CTGCGTCTAC 60
 CGTGAGGATT TCAAGCGACT GCTGCTAACC CCGGTATACT CGGTGGTGCT GGTGGTCGGC 120
 CTGCCACTGA ACATCTGCGT CATTGCCCAG ATCTGCGCAT CCCGCCGGAC CCTGACCCGT 180
 TCCGCTGTGT ACACCCTGAA CCTGGCACTG GCGGACCTGA TGTATGCCTG TCACTACCC 240
 CTACTTATCT ATA ACTACGC CAGAGGGGAC CACTGGCCCT TCGGAGACCT CGCCTGCCGC 300
 TTTGTACGCT TCCTCTTCTA TGCCAATCTA CATGGCAGCA TCCTGTTTCT CACCTGCATT 360

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AGCTTCCAGC GCTACCTGGG CATCTGCCAC CCCCTGGCTT CCTGGCACAA GCGTGGAGGT      420
CGCCGTGCTG CTTGGGTAGT GTGTGGAGTC GTGTGGCTGG CTGTGACAGC CCAGTGCCTG      480
CCCACGGCAG TCTTTGCTGC CACAGGCATC CAGCGCAACC GCACTGTGTG CTACGACCTG      540
AGCCCACCCA TCCTGTCTAC TCGCTACCTG CCCTATGGTA TGGCCCTCAC GGTCATCGGC      600
TTCTTGCTGC CCTTCATAGC CTTACTGGCT TGTTATTGTC GCATGGCCCG CCGCCTGTGT      660
CGCCAGGATG GCCCAGCAGG TCCTGTGGCC CAAGAGCGGC GCAGCAAGGC GGCTCGTATG      720
GCTGTGGTGG TGGCAGCTGT CTTTGCCATC AGCTTCCTGC CTTTCCACAT CACCAAGACA      780
GCCTACTTGG CTGTGCGCTC CACGCCCGGT GTCTCTTGCC CTGTGCTGGA GACCTTCGCT      840
GCTGCCTACA AAGGCACTCG GCCCTTCGCC AGTGTCAACA GTGTTCTGGA CCCCATTTCTC      900
TTCTACTTCA CACAACAGAA GTTCCGGCGG CAACCCCACG ATCTCTTACA GAGGCTCACA      960
GCCAAGTGGC AGAGGCAGAG AGTC                                             984

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(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ala Ala Met Ser Val Asp Arg Tyr Val Ala Ile Val His Ser Arg Arg
1 5 10 15

Ser Ser Ser Leu Arg Val Ser Arg Asn Ala Leu Leu Gly Val Gly Phe
20 25 30

Ile Trp Ala Leu Ser Ile Ala Met Ala Ser Pro Val Ala Tyr His Gln
35 40 45

Arg Leu Phe His Arg Asp Ser Asn Gln Thr Phe Cys Trp Glu Gln Trp
50 55 60

Pro Asn Lys Leu His Lys Lys Ala Tyr Val Val Cys Thr Phe Val Phe
65 70 75 80

Gly Tyr Leu Leu Pro Leu Leu Leu Ile Cys Phe Cys Tyr Ala Lys Val
85 90 95

Leu Asn His Leu His Lys Lys Leu Lys Asn Met Ser Lys Lys Ser Glu

100	105	110
Ala Ser Lys Lys Lys Thr Ala Gln Thr Val Leu Val Val Val Val		
115	120	125

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

E1

GCCGCGATGT CTGTGGATCG CTACGTGGCC ATTGTGCACT CGCGGCGCTC CTCCTCCCTC	60
AGGGTGTCCC GCAACGCACT GCTGGGCGTG GGCTTCATCT GGGCGCTGTC CATCGCCATG	120
GCCTCGCCGG TGGCCTACCA CCAGCGTCTT TTCCATCGGG ACAGCAACCA GACCTTCTGC	180
TGGGAGCAGT GGCCCAACAA GCTCCACAAG AAGGCTTACG TGGTGTGCAC TTTCGTCTTT	240
GGGTACCTTC TGCCCTTACT GCTCATCTGC TTTTGCTATG CCAAGGTCCT TAATCATCTG	300
CATAAAAAGC TGAAAAACAT GTCAAAAAG TCTGAAGCAT CCAAGAAAAA GACTGCACAG	360
ACCGTCCTGG TGGTCGTTGT AGTA	384

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Val Leu Trp Phe Phe Gly Phe Ser Ile Lys Arg Thr Pro Phe Ser Val	
1 5 10 15	
Tyr Phe Leu His Leu Ala Ser Ala Asp Gly Ala Tyr Leu Phe Ser Lys	
20 25 30	
Ala Val Phe Ser Leu Leu Asn Ala Gly Gly Phe Leu Gly Thr Phe Ala	
35 40 45	

His Tyr Val Arg Ser Val Ala Arg Val Leu Gly Leu Cys Ala Phe Val
 50 55 60

Ala Gly Val Ser Leu Leu Pro
 65 70

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTGCTCTGGT TCTTCGGCTT CTCCATCAAG AGGACCCCCT TCTCCGTCTA CTCCTGCAC 60
 CTGGCCAGCG CCGACGGCGC CTACCTCTTC AGCAAGGCCG TGTTCTCCCT GCTGAACGCC 120
 GCGGGCTTCC TGGGCACCTT CGCCCACTAT GTGCGCAGCG TGGCCCGGGT GCTGGGGCTC 180
 TGC GCCTTCG TGGCGGGCGT GAGCCTCCTG CCGGC 215

E1

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Glu Leu Ala Met Val Asn Leu Ser Glu Gly Asn Gly Ser Asp Pro
 1 5 10 15
 Glu Pro Pro Ala Pro Glu Ser Arg Pro Leu Phe Gly Ile Gly Val Glu
 20 25 30
 Asn Phe Ile Thr Leu Val Val Phe Gly Leu Ile Phe Ala Met Gly Val
 35 40 45
 Leu Gly Asn Ser Leu Val Ile Thr Val Leu Ala Arg Ser Lys Pro Gly
 50 55 60
 Lys Pro Arg Ser Thr Thr Asn Leu Phe Ile Leu Asn Leu Ser Ile Ala
 65 70 75 80

Asp Leu Ala Tyr Leu Leu Phe Cys Ile Pro Phe Gln Ala Thr Val Tyr
 85 90 95
 Ala Leu Pro Thr Trp Val Leu Gly Ala Phe Ile Cys Lys Phe Ile His
 100 105 110
 Tyr Phe Phe Thr Val Ser Met Leu Val Ser Ile Phe Thr Leu Ala Ala
 115 120 125
 Met Ser Val Asp Arg Tyr Val Ala Ile Val His Ser Arg Arg Ser Ser
 130 135 140
 Ser Leu Arg Val Ser Arg Asn Ala Leu Leu Gly Val Gly Phe Ile Trp
 145 150 155 160
 Ala Leu Ser Ile Ala Met Ala Ser Pro Val Ala Tyr His Gln Arg Leu
 165 170 175
 Phe His Arg Asp Ser Asn Gln Thr Phe Cys Trp Glu Gln Trp Pro Asn
 180 185 190
 Lys Leu His Lys Lys Ala Tyr Val Val Cys Thr Phe Val Phe Gly Tyr
 195 200 205
 Leu Leu Pro Leu Leu Leu Ile Cys Phe Cys Tyr Ala Lys Val Leu Asn
 210 215 220
 His Leu His Lys Lys Leu Lys Asn Met Ser Lys Lys Ser Glu Ala Ser
 225 230 235 240
 Lys Lys Lys Thr Ala Gln Thr Val Leu Val Val Val Val Val Phe Gly
 245 250 255
 Ile Ser Trp Leu Pro His His Val Val His Leu Trp Ala Glu Phe Gly
 260 265 270
 Ala Phe Pro Leu Thr Pro Ala Ser Phe Phe Phe Arg Ile Thr Ala His
 275 280 285
 Cys Leu Ala Tyr Ser Asn Ser Ser Val Asn Pro Ile Ile Tyr Ala Phe
 290 295 300
 Leu Ser Glu Asn Phe Arg Lys Ala Tyr Lys Gln Val Phe Lys Cys His
 305 310 315 320
 Val Cys Asp Glu Ser Pro Arg Ser Glu Thr Lys Glu Asn Lys Ser Arg
 325 330 335
 Met Asp Thr Pro Pro Ser Thr Asn Cys Thr His Val
 340 345

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1044 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATGGAAGTGG CTATGGTGAA CCTCAGTGAA GGAATGGGA GCGACCCAGA GCCGCCAGCC 60

CCGGAGTCCA GGCCGCTCTT CGGCATTGGC GTGGAGAACT TCATTACGCT GGTAGTGTTT 120

GGCCTGATTT TCGCGATGGG CGTGCTGGGC AACAGCCTGG TGATCACCGT GCTGGCGCGC 180

AGCAAACCAG GCAACCCCCG CAGCACCACC AACCTGTTTA TCCTCAATCT GAGCATCGCA 240

GACCTGGCCT ACCTGCTCTT CTGCATCCCT TTTCAGGCCA CCGTGTATGC ACTGCCCACC 300

TGGGTGCTGG GCGCCTTCAT CTGCAAGTTT ATACACTACT TCTTCACCGT GTCCATGCTG 360

GTGAGCATCT TCACCCTGGC CGCGATGTCT GTGGATCGCT ACGTGGCCAT TGTGCACTCG 420

CGGCGCTCCT CCTCCCTCAG GGTGTCCCGC AACGCACTGC TGGGCGTGGG CTCATCTGG 480

GCGCTGTCCA TCGCCATGGC CTCGCCGGTG GCCTACCACC AGCGTCTTTT CCATCGGGAC 540

AGCAACCAGA CCTTCTGCTG GGAGCAGTGG CCCAACAAGC TCCACAAGAA GGCTTACGTG 600

GTGTGCACTT TCGTCTTTGG GTACCTTCTG CCCTTACTGC TCATCTGCTT TTGCTATGCC 660

AAGGTCCTTA ATCATCTGCA TAAAAAGCTG AAAAACATGT CAAAAAAGTC TGAAGCATCC 720

AAGAAAAAGA CTGCACAGAC CGTCCTGGTG GTCGTTGTAG TATTTGGCAT ATCCTGGCTG 780

CCCCATCATG TCGTCCACCT CTGGGCTGAG TTTGGAGCCT TCCCACTGAC GCCAGCTTCC 840

TTCTTCTTCA GAATCACCGC CCATTGCCTG GCATACAGCA ACTCCTCAGT GAACCCCATC 900

ATATATGCCT TTCTCTCAGA AAACCTCCGG AAGGCGTACA AGCAAGTGTT CAAGTGTCAT 960

GTTTGCGATG AATCTCCACG CAGTGAAACT AAGGAAAACA AGAGCCGGAT GGACACCCCG 1020

CCATCCACCA ACTGCACCCA CGTG 1044

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu Leu Thr Leu His Pro Val Trp Ser Gln Lys His Arg Thr Ser His
 1 5 10 15
 Trp Ala Ser Arg Val Val Leu Gly Val Trp Leu Ser Ala Thr Ala Phe
 20 25 30
 Ser Val Pro Tyr Leu Val Phe Arg Glu Thr Tyr Asp Asp Arg Lys Gly
 35 40 45
 Arg Val Thr Cys Arg Asn Asn Tyr Ala Val Ser Thr Asp Trp Glu Ser
 50 55 60
 Lys Glu Met Gln Thr Val Arg Gln Trp Ile His Ala Thr Cys Phe Ile
 65 70 75 80
 Ser Arg Phe Ile Leu Gly Phe Leu Leu Pro Phe Leu Val Ile Gly Phe
 85 90 95
 Cys Tyr Glu Arg Val Ala Arg Lys Met Lys Glu Arg Gly Leu Phe Lys
 100 105 110
 Ser Ser Lys Pro Phe Lys Val Thr Met Thr Ala Val Ile
 115 120 125

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTTCTCACCC TTCACCCAGT GTGGTCCCAA AAGCACCGAA CCTCACACTG GGCTTCCAGA 60
 GTCGTTCTGG GAGTCTGGCT CTCTGCCACT GCCTTCAGCG TGCCCTATTT GGTTTTCAGG 120
 GAGACATATG ATGACCGTAA AGGAAGAGTG ACCTGCAGAA ATAACCTACGC TGTGTCCACT 180
 GACTGGGAAA GCAAAGAGAT GCAAACAGTA AGACAATGGA TTCATGCCAC CTGTTTCATC 240
 AGCCGCTTCA TACTGGGCTT CCTTCTGCCT TTCTTAGTCA TTGGCTTTTG TTATGAAAGA 300
 GTAGCCCGCA AGATGAAAGA GAGGGGCCTC TTAAATCCA GCAAACCCTT CAAAGTCACG 360
 ATGACTGCTG TTATCTC 377

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Phe Lys Ile Val Lys Pro Leu Ser Thr Ser Phe Ile Gln Ser Val Asn
 1 5 10 15
 Tyr Ser Lys Leu Val Ser Leu Val Val Trp Leu Leu Met Leu Leu Leu
 20 25 30
 Ala Val Pro Asn Val Ile Leu Thr Asn Gln Arg Val Lys Asp Val Thr
 35 40 45
 Gln Ile Lys Cys Met Glu Leu Lys Asn Glu Leu Gly Arg Gln Trp His
 50 55 60
 Lys Ala Ser Asn Tyr Ile Phe Val Gly Ile Phe Trp Leu Val Phe Leu
 65 70 75 80
 Leu Leu Ile Ile Phe Tyr Thr Ala Ile Thr Arg Lys Ile Phe Lys Ser
 85 90 95
 His Leu Lys Ser Arg Lys Asn Ser Ile Ser Val Lys Lys Lys Ser Ser
 100 105 110
 Arg Asn Ile Phe Ser Ile Val
 115

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTCAAGATTG TGAAGCCCCT TTCCACGTCC TTCATCCAGT CTGTGAACTA CAGCAAACCTC 60
 GTCTCGCTGG TGGTCTGGTT GCTCATGCTC CTCCTCGCCG TCCCCAACGT CATTCTCACC 120

AACCAGAGAG TTAAGGACGT GACGCAGATA AAATGCATGG AACTTAAAAA CGAACTGGGC 180
 CGCCAGTGGC ACAAGGCGTC AACTACATC TTTGTGGGCA TTTTCTGGCT TGTGTTCCTT 240
 TTGCTAATCA TTTTCTACAC TGCTATCACC AGGAAAATCT TTAAGTCCCA CCTGAAATCC 300
 AGAAAGAATT CCATCTCGGT CAAAAGAAA TCTAGCCGCA ACATCTTCAG CATCGTG 357

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Val Asp Leu Leu Ala Ala Leu Thr Leu Met Pro Leu Ala Met Leu Ser
 1 5 10 15
 Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly Glu Val Ala Cys Arg
 20 25 30
 Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu Ala Ile Leu Ser
 35 40 45
 Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Tyr Val Val His Pro Met
 50 55 60
 Arg Tyr Glu Val Arg Met Lys Leu Gly Leu Val Ala Ser Val Leu Val
 65 70 75 80
 Gly Val Trp Val Lys Ala Leu Ala Met Ala Ser Val Pro Val Leu Gly
 85 90 95
 Arg Val Ser Trp Glu Glu Gly Pro Pro Ser Val Pro Pro Gly Cys Ser
 100 105 110
 Leu Gln Trp Ser His Ser Ala Tyr Cys Gln Leu Phe Val Val Val Phe
 115 120 125
 Ala Val Leu Tyr Phe Leu Leu Pro Leu Leu Leu Ile Leu Val Val Tyr
 130 135 140
 Cys Ser Met Phe Arg Val Ala Arg Val Ala Ala Met Gln His Gly Pro
 145 150 155 160
 Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg Ser Glu Ser Leu Ser
 165 170 175

Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro Gln Thr Thr Pro
 180 185 190

His Arg Thr Phe Gly Gly Gly Lys Ala Ala Val Val Leu Leu Ala Val
 195 200 205

Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe Ser Phe His Leu
 210 215 220

Tyr Val Ala Leu Ser Ala Gln Pro Ile Ala Ala Gly Gln Val Glu Asn
 225 230 235 240

Val Val Thr Trp Ile Gly Tyr Phe Cys Phe Thr Ser
 245 250

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GTGGACCTGC TGGCTGCCCT GACCCTCATG CCTCTGGCCA TGCTCTCCAG CTCCGCCCTC 60

TTTGACCACG CCCTCTTTGG GGAGGTGGCC TGCCGCCTCT ACTTGTTTCCT GAGCGTCTGC 120

TTTGTCAGCC TGGCCATCCT CTCGGTGTCC GCCATCAATG TGGAGCGCTA CTATTATGTG 180

GTCCACCCCA TGCCTATGA GGTGCGCATG AAAGTGGGGC TGGTGGCCTC TGTGCTGGTG 240

GGCGTGTGGG TGAAGGCCCT GGCCATGGCT TCTGTGCCAG TGTTGGGAAG GGTGTCCTGG 300

GAGGAAGGCC CTCCCAGTGT CCCCCAGGC TGTTCACTCC AATGGAGCCA CAGTGCCTAC 360

TGCCAGCTTT TCGTGGTGGT CTTGCGCGTC CTCTACTTCC TGCTGCCCCT GCTCCTCATC 420

CTTGTGGTCT ACTGCAGCAT GTTCCGGGTG GCTCGTGTGG CTGCCATGCA GCACGGGCCG 480

CTGCCCACGT GGATGGAGAC GCCCCGGCAA CGCTCCGAGT CTCTCAGCAG CCGCTCCACT 540

ATGGTCACCA GCTCGGGGGC CCCGCAGACC ACCCCTCACC GGACGTTTGG CGGAGGGAAG 600

GCAGCAGTGG TCCTCCTGGC TGTGGGAGGA CAGTTCCTGC TCTGTTGGTT GCCCTACTTC 660

TCCTTCCACC TCTATGTGGC CCTGAGCGCT CAGCCCATTG CAGCGGGGCA GGTGGAGAAC 720

GTGGTGACCT GGATTGGCTA CTTCTGCTTC ACCTCC 756

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ala Asp Val Leu Val Thr Ala Ile Cys Leu Pro Ala Ser Leu Leu Val
 1 5 10 15

Asp Ile Thr Glu Ser Trp Leu Phe Gly His Ala Leu Cys Lys Val Ile
 20 25 30

Pro Tyr Leu Gln Ala Val Ser Val Ser Val Val Val Leu Thr Leu Ser
 35 40 45

Ser Ile Ala Leu Asp Arg Trp Tyr Ala Ile Cys His Pro Leu Leu Phe
 50 55 60

Lys Ser Thr Ala Arg Arg Ala Arg Gly Ser Ile Leu Gly Ile Trp Ala
 65 70 75 80

Val Ser Leu Ala Val Met Val Pro Gln Ala Ala Val Met Glu Cys Ser
 85 90 95

Ser Val Leu Pro Glu Leu Ala Asn Arg Thr Arg Leu Leu Ser Val Cys
 100 105 110

Asp Glu Arg Trp Ala Asp Asp Leu Tyr Pro Lys Ile Tyr His Ser Cys
 115 120 125

Phe Phe Ile Val Thr Tyr Leu Ala Pro Leu Gly Leu Met Ala Met Ala
 130 135 140

Tyr Phe Gln Ile Phe Arg Lys Leu Trp Gly Arg Gln Ile Pro Gly Thr
 145 150 155 160

Thr Ser Ala Leu Val Arg Asn Trp Lys Arg Pro Ser Asp Gln Leu Asp
 165 170 175

Asp Gln Gly Gln Gly Leu Ser Ser Glu Pro Gln Pro Arg Ala Arg Ala
 180 185 190

Phe Leu Ala Glu Val Lys Gln Met Arg Ala Arg Arg Lys Thr Ala Lys
 195 200 205

Met Leu Met Val Val Leu Leu Val Phe Ala Leu Cys Tyr Leu Pro Ile

E1

210	215	220
Ser Val Leu Asn Val Leu Lys Arg Val Phe Gly Met Phe Arg Gln Ala		
225	230	235 240
Ser Asp Arg Glu Ala Ile Tyr Ala Cys Phe Thr Phe Ser His Trp Leu		
	245	250 255
Val Tyr Ala Asn Ser Ala Ala		
	260	

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

E1

GCCGATGTGC TGGTGACAGC CATCTGCCTG CCGGCCAGTC TGCTGGTAGA CATCACGGAA	60
TCCTGGCTCT TTGGCCATGC CCTCTGCAAG GTCATCCCCT ATCTACAGGC CGTGTCCGTG	120
TCAGTGGTCG TGCTGACTCT CAGCTCCATC GCCCTGGACC GCTGGTACGC CATCTGCCAC	180
CCGCTGTTGT TCAAGAGCAC TGCCCGGCGC GCCCGCGGCT CCATCCTCGG CATCTGGGCG	240
GTGTCGCTGG CTGTCATGGT GCCTCAGGCT GCTGTCATGG AGTGTAGCAG CGTGCTGCCC	300
GAGCTGGCCA ACCGCACCCG CCTCCTGTCT GTCTGTGATG AGCGCTGGGC AGACGACCTG	360
TACCCCAAGA TCTACCACAG CTGCTTCTTC ATTGTCACCT ACCTGGCCCC ACTGGGCCTC	420
ATGGCCATGG CCTATTTCCA GATCTTCCGC AAGCTCTGGG GCCGCCAGAT CCCCGGCACC	480
ACCTCGGCCC TGGTGCGCAA CTGGAAGCGG CCCTCAGACC AGCTGGACGA CCAGGGCCAG	540
GGCCTGAGCT CAGAGCCCCA GCCCCGGGCC CGCGCCTTCC TGGCCGAGGT GAAACAGATG	600
CGAGCCCGGA GGAAGACGGC CAAGATGCTG ATGGTGGTGC TGCTGGTCTT CGCCCTCTGC	660
TACCTGCCCCA TCAGTGTCTT CAACGTCCTC AAGAGGGTCT TCGGGATGTT CCGCCAAGCC	720
AGCGACCGAG AGGCCATCTA CGCCTGCTTC ACCTTCTCCC ACTGGCTGGT GTACGCCAAC	780
AGCGCCGCC	789

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Glu Trp Asp Asn Gly Thr Gly Gln Ala Leu Gly Leu Pro Pro Thr
 1 5 10 15

Thr Cys Val Tyr Arg Glu Asn Phe Lys Gln Leu Leu Leu Pro Pro Val
 20 25 30

Tyr Ser Ala Val Leu Ala Ala Gly Leu Pro Leu Asn Ile Cys Val Ile
 35 40 45

Thr Gln Ile Cys Thr Ser Arg Arg Ala Leu Thr Arg Thr Ala Val Tyr
 50 55 60

Thr Leu Asn Leu Ala Leu Ala Asp Leu Leu Tyr Ala Cys Ser Leu Pro
 65 70 75 80

Leu Leu Ile Tyr Asn Tyr Ala Gln Gly Asp His Trp Pro Phe Gly Asp
 85 90 95

Phe Ala Cys Arg Leu Val Arg Phe Leu Phe Tyr Ala Asn Leu His Gly
 100 105 110

Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly Ile
 115 120 125

Cys His Pro Leu Ala Pro Trp His Lys Arg Gly Gly Arg Arg Ala Ala
 130 135 140

Trp Leu Val Cys Val Thr Val Trp Leu Ala Val Thr Thr Gln Cys Leu
 145 150 155 160

Pro Thr Ala Ile Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val
 165 170 175

Cys Tyr Asp Leu Ser Pro Pro Ala Leu Ala Thr His Tyr Met Pro Tyr
 180 185 190

Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ala Ala Leu
 195 200 205

Leu Ala Cys Tyr Cys Leu Leu Ala Cys Arg Leu Cys Arg Gln Asp Gly
 210 215 220

Pro Ala Glu Pro Val Ala Gln Glu Arg Arg Gly Lys Ala Ala Arg Met

225		230		235		240
Ala Val Val Val	Ala Ala Ala Phe	Ala Ile Ser Phe	Leu Pro Phe	His		
	245		250		255	
Ile Thr Lys Thr	Ala Tyr Leu Ala	Val Gly Ser Thr	Pro Gly Val	Pro		
	260		265		270	
Cys Thr Val Leu	Glu Ala Phe Ala	Ala Ala Tyr Lys	Gly Thr Arg	Pro		
	275		280		285	
Phe Ala Ser Ala	Asn Ser Val Leu	Asp Pro Ile Leu	Phe Tyr Phe	Thr		
	290		295		300	
Gln Lys Lys Phe	Arg Arg Arg Pro	His Glu Leu Leu	Gln Lys Leu	Thr		
305		310		315		320
Ala Lys Trp Gln	Arg Gln Gly Arg					
	325					

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATGGAATGGG ACAATGGCAC AGGCCAGGCT CTGGGCTTGC CACCCACCAC CTGTGTCTAC	60
CGCGAGAACT TCAAGCAACT GCTGCTGCCA CCTGTGTATT CGGCGGTGCT GGCGGCTGGC	120
CTGCCGCTGA ACATCTGTGT CATTACCCAG ATCTGCACGT CCCGCCGGGC CCTGACCCGC	180
ACGGCCGTGT ACACCCTAAA CCTTGCTCTG GCTGACCTGC TATATGCCTG CTCCTGCCC	240
CTGCTCATCT ACAACTATGC CCAAGGTGAT CACTGGCCCT TTGGCGACTT CGCCTGCCGC	300
CTGGTCCGCT TCCTCTTCTA TGCCAACCTG CACGGCAGCA TCCTCTTCCT CACCTGCATC	360
AGCTTCCAGC GCTACCTGGG CATCTGCCAC CCGCTGGCCC CCTGGCACAA ACGTGGGGGC	420
CGCCGGGCTG CCTGGCTAGT GTGTGTAACC GTGTGGCTGG CCGTGACAAC CCAGTGCCTG	480
CCCACAGCCA TCTTCGCTGC CACAGGCATC CAGCGTAACC GCACTGTCTG CTATGACCTC	540
AGCCCGCCTG CCCTGGCCAC CCACTATATG CCCTATGGCA TGGCTCTCAC TGTCATCGGC	600
TTCCTGCTGC CCTTTGCTGC CCTGCTGGCC TGCTACTGTC TCCTGGCCTG CCGCCTGTGC	660

CGCCAGGATG GCCCGGCAGA GCCTGTGGCC CAGGAGCGGC GTGGCAAGGC GGCCCGCATG	720
GCCGTGGTGG TGGCTGCTGC CTTTGCCATC AGCTTCCTGC CTTTTCACAT CACCAAGACA	780
GCCTACCTGG CAGTGGGCTC GACGCCGGGC GTCCCCTGCA CTGTATTGGA GGCCTTTGCA	840
GCGGCCTACA AAGGCACGCG GCCGTTTGCC AGTGCCAACA GCGTGCTGGA CCCCATCCTC	900
TTCTACTTCA CCCAGAAGAA GTTCCGCCGG CGACCACATG AGCTCCTACA GAAACTCACA	960
GCCAAATGGC AGAGGCAGGG TCGC	984

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGCCATCT TCGCTGCCAC AGGCAT 26

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AGACAGTAGC AGGCCAGCAG GGCAGCAAA 29

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA

(ix) FEATURE:

(D)OTHER INFORMATION:/note= N is inosine; Y is C or T; S is G or C;
K is G or T; M is A or C."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CTGTGYGYSA TYGCNNTKGA YMGSTAC

27

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

((ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA

(ix) FEATURE:

(D)OTHER INFORMATION:/note= N is inosine; S is G or C; W is A or T;
R is A or G; K is G or T; Y is C or T."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AKGWAGWAGG GCAGCCAGCA GANSRYGAA

29